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1600

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/652,292C

DATE: 05/06/2003
TIME: 12:01:33

Input Set : A:\EP.txt
Output Set: N:\CRF4\05062003\I652292C.raw

3 <110> APPLICANT: Bowden, Donald W.
4 Dawson, Paul A.
5 Fossey, Sallyanne C.
7 <120> TITLE OF INVENTION: GLUT10: A Novel Glucose Transporter in the Type 2 Diabetes
Linked
8 Region of Chromosome 20Q12-13.1
10 <130> FILE REFERENCE: 9151-11
12 <140> CURRENT APPLICATION NUMBER: US 09/652,292C
13 <141> CURRENT FILING DATE: 2000-08-31
15 <160> NUMBER OF SEQ ID NOS: 43
17 <170> SOFTWARE: PatentIn version 3.2
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 4395
21 <212> TYPE: DNA
22 <213> ORGANISM: Homo sapiens
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34 cagggcagga gggacagagg cggggggcggg ccggaaagtt tgcggcgcc cagccgcgtt 180
36 ggggactccg gcggggatcg cgcgcggcc ccctcagcgc cccagcaca g cgcggagtc 240
38 ccgcgtgcc atg ggc cac tcc cca cct gtc ctg cct ttg tgt gcc tct gtg 291
39 Met Gly His Ser Pro Pro Val Leu Pro Leu Cys Ala Ser Val
40 1 5 10
42 tct ttg ctg ggt ggc ctg acc ttt ggt tat gaa ctg gca gtc ata tca 339
43 Ser Leu Leu Gly Gly Leu Thr Phe Gly Tyr Glu Leu Ala Val Ile Ser
44 15 20 25 30
46 ggt gcc ctg ctg cca ctg cag ctt gac ttt ggg cta agc tgc ttg gag 387
47 Gly Ala Leu Leu Pro Leu Gln Leu Asp Phe Gly Leu Ser Cys Leu Glu
48 35 40 45
50 cag gag ttc ctg gtg ggc agc ctg ctc ctg ggg gct ctc ctc gcc tcc 435
51 Gln Glu Phe Leu Val Gly Ser Leu Leu Gly Ala Leu Leu Ala Ser
52 50 55 60
54 ctg gtt ggt ggc ttc ctc att gac tgc tat ggc agg aag caa gcc atc 483
55 Leu Val Gly Gly Phe Leu Ile Asp Cys Tyr Gly Arg Lys Gln Ala Ile
56 65 70 75
58 ctc ggg agc aac ttg gtg ctg ctg gca ggc agc ctg acc ctg ggc ctg 531
59 Leu Gly Ser Asn Leu Val Leu Leu Ala Gly Ser Leu Thr Leu Gly Leu
60 80 85 90
62 gct ggt tcc ctg gcc tgg ctg gtc ctg ggc cgc gct gtg gtt ggc ttc 579
63 Ala Gly Ser Leu Ala Trp Leu Val Leu Gly Arg Ala Val Val Gly Phe
64 95 100 105 110

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71	Val	Gly	Pro	Arg	Gln	Arg	Gly	Val	Leu	Val	Ser	Leu	Tyr	Glu	Ala	Gly	
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74	atc	acc	gtg	ggc	atc	ctg	ctc	tcc	tat	gcc	ctc	aac	tat	gca	ctg	723	
75	Ile	Thr	Val	Gly	Ile	Leu	Leu	Ser	Tyr	Ala	Leu	Asn	Tyr	Ala	Leu	Ala	
76								145		150					155		
78	ggt	acc	ccc	tgg	gg	tgg	agg	cac	atg	ttc	ggc	tgg	gcc	act	gca	771	
79	Gly	Thr	Pro	Trp	Gly	Trp	Arg	His	Met	Phe	Gly	Trp	Ala	Thr	Ala	Pro	
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82	gct	gtc	ctg	caa	tcc	ctc	agc	ctc	ctc	ctc	cct	gct	ggt	aca	gat	819	
83	Ala	Val	Leu	Gln	Ser	Leu	Ser	Leu	Leu	Phe	Leu	Pro	Ala	Gly	Thr	Asp	
84								175		180					190		
86	gag	act	gca	aca	cac	aag	gac	ctc	atc	cca	ctc	cag	gg	ggt	gag	867	
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92								210		215					220		
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95	Arg	Ala	Arg	Asp	Asn	Met	Arg	Gly	Arg	Thr	Thr	Val	Gly	Leu	Gly	Leu	
96								225		230					235		
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110	gcc	atg	ggg	ctg	gtg	gac	cgt	gca	ggc	cgc	agg	gct	ctg	ttg	cta	gct	1155
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114	ggc	tgt	gcc	ctc	atg	gcc	ctg	tcc	gt	agt	ggc	ata	ggc	ctc	gtc	agc	1203
115	Gly	Cys	Ala	Leu	Met	Ala	Leu	Ser	Val	Ser	Gly	Ile	Gly	Leu	Val	Ser	
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118	ttt	gcc	gtg	ccc	atg	gac	tca	ggc	cca	agc	tgt	ctg	gct	gtg	ccc	aat	1251
119	Phe	Ala	Val	Pro	Met	Asp	Ser	Gly	Pro	Ser	Cys	Leu	Ala	Val	Pro	Asn	
120								320		325					330		
122	gcc	acc	ggg	cag	aca	ggc	ctc	cct	gg	gac	tct	ggc	ctg	ctg	cag	gac	1299
123	Ala	Thr	Gly	Gln	Thr	Gly	Leu	Pro	Gly	Asp	Ser	Gly	Leu	Leu	Gln	Asp	
124								335		340					345		350
126	tcc	tct	cta	cct	ccc	att	cca	agg	acc	aat	gag	gac	caa	agg	gag	cca	1347
127	Ser	Ser	Leu	Pro	Pro	Ile	Pro	Arg	Thr	Asn	Glu	Asp	Gln	Arg	Glu	Pro	
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130	atc	ttg	tcc	act	gt	aag	aaa	acc	aag	ccc	cat	ccc	aga	tct	gga	gac	1395

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135	Pro	Ser	Ala	Pro	Pro	Arg	Leu	Ala	Leu	Ser	Ser	Ala	Leu	Pro	Gly	Pro	
136					385			390							395		
138	cct	ctg	ccc	gct	cg	ggg	cat	gca	ctg	ctg	cg	tgg	acc	gca	ctg	ctg	1491
139	Pro	Leu	Pro	Ala	Arg	Gly	His	Ala	Leu	Leu	Arg	Trp	Thr	Ala	Leu	Leu	
140					400			405							410		
142	tgc	ctg	atg	gtc	ttt	gtc	agt	gcc	ttc	tcc	ttt	ggg	ttt	ggg	cca	gtg	1539
143	Cys	Leu	Met	Val	Phe	Val	Ser	Ala	Phe	Ser	Phe	Gly	Phe	Gly	Pro	Val	
144	415				420						425				430		
146	acc	tgg	ctt	gtc	ctc	agc	gag	atc	tac	cct	gtg	gag	ata	cga	gga	aga	1587
147	Thr	Trp	Leu	Val	Leu	Ser	Glu	Ile	Tyr	Pro	Val	Glu	Ile	Arg	Gly	Arg	
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152					450			455							460		
154	agc	ctc	tcc	ttc	ctc	gat	ctc	att	ggc	acc	atc	ggc	ttg	tcc	tgg	acc	1683
155	Ser	Leu	Ser	Phe	Leu	Asp	Leu	Ile	Gly	Thr	Ile	Gly	Leu	Ser	Trp	Thr	
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238	agtatgt	ctt	tttgc	tttgc	aaat	atgtt	gtat	accc	ggg	at	tttgc	3855		
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242	gag	tttgc	at	tgc	tttgc	at	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	3975
244	tttca	acc	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	4035
246	cagg	gat	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	4095
248	actt	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	4155
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254	caca	aaaa	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	4335
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260 <211> LENGTH: 541
261 <212> TYPE: PRT

262 <213> ORGANISM: Homo sapiens

264 <400> SEQUENCE: 2

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271					20				25						30		
274	Leu	Leu	Pro	Leu	Gln	Leu	Asp	Phe	Gly	Leu	Ser	Cys	Leu	Glu	Gln	Glu	
275					35				40						45		
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279					50				55						60		
282	Gly	Gly	Phe	Leu	Ile	Asp	Cys	Tyr	Gly	Arg	Lys	Gln	Ala	Ile	Leu	Gly	
283					65				70						75		80
286	Ser	Asn	Leu	Val	Leu	Leu	Ala	Gly	Ser	Leu	Thr	Leu	Gly	Leu	Ala	Gly	
287									85						90		95
290	Ser	Leu	Ala	Trp	Leu	Val	Leu	Gly	Arg	Ala	Val	Val	Gly	Phe	Ala	Ile	
291									100						105		110
294	Ser	Leu	Ser	Ser	Met	Ala	Cys	Cys	Ile	Tyr	Val	Ser	Glu	Leu	Val	Gly	
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298	Pro	Arg	Gln	Arg	Gly	Val	Leu	Val	Ser	Leu	Tyr	Glu	Ala	Gly	Ile	Thr	
299									130						135		140
302	Val	Gly	Ile	Leu	Leu	Ser	Tyr	Ala	Leu	Asn	Tyr	Ala	Leu	Ala	Gly	Thr	

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311	180	185	190	
314	Ala Thr His Lys Asp Leu Ile Pro Leu Gln Gly Gly Glu Ala Pro Lys			
315	195	200	205	
318	Leu Gly Pro Gly Arg Pro Arg Tyr Ser Phe Leu Asp Leu Phe Arg Ala			
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322	Arg Asp Asn Met Arg Gly Arg Thr Thr Val Gly Leu Gly Leu Val Leu			
323	225	230	235	240
326	Phe Gln Gln Leu Thr Gly Gln Pro Asn Val Leu Cys Tyr Ala Ser Thr			
327	245	250	255	
330	Ile Phe Ser Ser Val Gly Phe His Gly Gly Ser Ser Ala Val Leu Ala			
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334	Ser Val Gly Leu Gly Ala Val Lys Val Ala Ala Thr Leu Thr Ala Met			
335	275	280	285	
338	Gly Leu Val Asp Arg Ala Gly Arg Arg Ala Leu Leu Leu Ala Gly Cys			
339	290	295	300	
342	Ala Leu Met Ala Leu Ser Val Ser Gly Ile Gly Leu Val Ser Phe Ala			
343	305	310	315	320
346	Val Pro Met Asp Ser Gly Pro Ser Cys Leu Ala Val Pro Asn Ala Thr			
347	325	330	335	
350	Gly Gln Thr Gly Leu Pro Gly Asp Ser Gly Leu Leu Gln Asp Ser Ser			
351	340	345	350	
354	Leu Pro Pro Ile Pro Arg Thr Asn Glu Asp Gln Arg Glu Pro Ile Leu			
355	355	360	365	
358	Ser Thr Ala Lys Lys Thr Lys Pro His Pro Arg Ser Gly Asp Pro Ser			
359	370	375	380	
362	Ala Pro Pro Arg Leu Ala Leu Ser Ser Ala Leu Pro Gly Pro Pro Leu			
363	385	390	395	400
366	Pro Ala Arg Gly His Ala Leu Leu Arg Trp Thr Ala Leu Leu Cys Leu			
367	405	410	415	
370	Met Val Phe Val Ser Ala Phe Ser Phe Gly Phe Gly Pro Val Thr Trp			
371	420	425	430	
374	Leu Val Leu Ser Glu Ile Tyr Pro Val Glu Ile Arg Gly Arg Ala Phe			
375	435	440	445	
378	Ala Phe Cys Asn Ser Phe Asn Trp Ala Ala Asn Leu Phe Ile Ser Leu			
379	450	455	460	
382	Ser Phe Leu Asp Leu Ile Gly Thr Ile Gly Leu Ser Trp Thr Phe Leu			
383	465	470	475	480
386	Leu Tyr Gly Leu Thr Ala Val Leu Gly Leu Gly Phe Ile Tyr Leu Phe			
387	485	490	495	
390	Val Pro Glu Thr Lys Gly Gln Ser Leu Ala Glu Ile Asp Gln Gln Phe			
391	500	505	510	
394	Gln Lys Arg Arg Phe Thr Leu Ser Phe Gly His Arg Gln Asn Ser Thr			
395	515	520	525	
398	Gly Ile Pro Tyr Ser Arg Ile Glu Ile Ser Ala Ala Ser			
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